ELSEVIER

Biophysical Chemistry 64 (1997) 289–290

Biophysical Chemistry

Author Index to Volume 64

Ackers, G.K. and Bolen, D.W.
The Gibbs conference on biothermodynamics: Origins and evolution (64) 3
Ackers, G.K., see Doyle, M.L. (64) 271
Ackers, G.K., see Huang, Y. (64) 157
Allewell, N.M., see LiCata, V.J. (64) 225

Barany, G., see Barbar, E. (64) 45
Barbar, E., LiCata, V.J., Barany, G. and Woodward, C.
Local fluctuations and global unfolding of partially folded BPTI detected by NMR (64) 45
Beretta, S., see Gryczynski, Z. (64) 81
Bloomfield, V.A., see Rouzina, I. (64) 139
Bolen, D.W., see Ackers, G.K. (64) 3
Bucci, E., see Gryczynski, Z. (64) 81
Bujalowski, W., see Jezewska, M.J. (64) 253

Cai, G.-Z., Callaci, T.P., Luther, M.A. and Ching Lee, J.
Regulation of rabbit muscle phosphofructokinase by phosphorylation (64) 199
Callaci, T.P., see Cai, G.-Z. (64) 199
Chaiken, I.M., see Myszka, D.G. (64) 127
Chaires, J.B.
Possible origin of differences between van't Hoff and calorimetric enthalpy estimates (64) 15
Ching Lee, J., see Cai, G.-Z. (64) 199

DeKoster, G.T. and Robertson, A.D.
Calorimetrically-derived parameters for protein interactions with urea and guanidine–HCl are not consistent with denaturant m values (64) 59
Di Cera, E., see Guinto, E.R. (64) 103
Doyle, M.L., Holt, J.M. and Ackers, G.K.
Effects of NaCl on the linkages between O_2 binding and subunit assembly in human hemoglobin: titration of the quaternary enhancement effect (64) 271
Doyle, M.L., see Myszka, D.G. (64) 127
Dwyer, J.J., see García-Moreno E., B. (64) 211

Eftink, M.R. and Ionescu, R.
Thermodynamics of protein unfolding: questions pertinent to testing the validity of the two-state model (64) 175

Fang, J., see Ferrari, M.E. (64) 235
Ferrari, M.E., Fang, J. and Lohman, T.M.
A mutation in *E. coli* SSB protein (W54S) alters intra-tetramer negative cooperativity and inter-tetramer positive cooperativity for single-stranded DNA binding (64) 235
Freire, E., see Hilser, V.J. (64) 69

García-Moreno E., B., Dwyer, J.J., Gittis, A.G., Lattman, E.E., Spencer, D.S. and Stites, W.E.
Experimental measurement of the effective dielectric in the hydrophobic core of a protein (64) 211
Gittis, A.G., see García-Moreno E., B. (64) 211
Gryczynski, I., see Gryczynski, Z. (64) 81
Gryczynski, Z., Beretta, S., Lubkowski, J., Razynska, A., Gryczynski, I. and Bucci, E.
Time-resolved fluorescence of hemoglobin species (64) 81
Guinto, E.R. and Di Cera, E.
Critical role of W60d in thrombin allosterism (64) 103

Hall, K.B., see Lu, J. (64) 111
Hilser, V.J., Townsend, B.D. and Freire, E.
Structure-based statistical thermodynamic analysis of T4 lysozyme mutants: structural mapping of cooperative interactions (64) 69
Holt, J.M., see Doyle, M.L. (64) 271
Huang, Y., Koestner, M.L. and Ackers, G.K.
Tertiary and quaternary chloride effects of the partially ligated (CN-met) hemoglobin intermediates (64) 157

Ionescu, R., see Eftink, M.R. (64) 175

Jezewska, M.J. and Bujalowski, W.
Quantitative analysis of ligand–macromolecule interactions using differential dynamic quenching of the ligand fluorescence to monitor the binding (64) 253

Koestner, M.L., see Huang, Y. (64) 157

Lattman, E.E., see García-Moreno E., B. (64) 211
LiCata, V.J. and Allewell, N.M.
Is substrate inhibition a consequence of allostery in aspartate transcarbamylase? (64) 225
LiCata, V.J., see Barbar, E. (64) 45
Liu, Y. and Sturtevant, J.M.
Significant discrepancies between van't Hoff and calorimetric enthalpies. III (64) 121

Lohman, T.M., see Ferrari, M.E. (64) 235
Lopez, M.M., see Makhatadze, G.I. (64) 93
Lu, J. and Hall, K.B.
Thermal unfolding of the N-terminal RNA binding domain of the human U1A protein studied by differential scanning calorimetry (64) 111
Lubkowski, J., see Gryczynski, Z. (64) 81
Luther, M.A., see Cai, G.-Z. (64) 199

Makhatadze, G.I., Lopez, M.M. and Privalov, P.L.
Heat capacities of protein functional groups (64) 93
Morton, T.A., see Myszka, D.G. (64) 127
Myszka, D.G., Morton, T.A., Doyle, M.L. and Chaiken, I.M.
Kinetic analysis of a protein antigen–antibody interaction limited by mass transport on an optical biosensor (64) 127

Privalov, P.L., see Makhatadze, G.I. (64) 93

Razynska, A., see Gryczynski, Z. (64) 81
Robertson, A.D., see DeKoster, G.T. (64) 59
Rouzina, I. and Bloomfield, V.A.
Competitive electrostatic binding of charged ligands to polyelectrolytes: practical approach using the non-linear Poisson–Boltzmann equation (64) 139

Schellman, J.A.
Thermodynamics, molecules and the Gibbs conference (64) 7
Spencer, D.S., see García-Moreno E., B. (64) 211
Stites, W.E., see García-Moreno E., B. (64) 211
Sturtevant, J.M., see Liu, Y. (64) 121

Timasheff, S.N., see Xie, G. (64) 25
Townsend, B.D., see Hilser, V.J. (64) 69

Woodward, C., see Barbar, E. (64) 45

Xie, G. and Timasheff, S.N.
The thermodynamic mechanism of protein stabilization by trehalose (64) 25

ELSEVIER

Biophysical Chemistry 64 (1997) 291–294

Biophysical Chemistry

Subject Index to Volume 64

Allosteric enzymes
Thrombin; Na^+; Site-directed mutagenesis (Guinto, E.R. (64) 103)

Allosteric regulation
Cooperativity; Hemoglobin intermediate; Subunit assembly (Huang, Y. (64) 157)

Phosphorylation; Self-association; Protein–protein interaction; Phosphofructokinase (Cai, G.-Z. (64) 199)

Avogadro's hypothesis
Gibbs conferences; Molecular mechanisms; Site-directed mutagenesis; Thermodynamics (Schellman, J.A. (64) 7)

BIAcore
Surface plasmon resonance; Biosensor; Mass transport; Kinetics; Protein–protein interaction (Myszka, D.G. (64) 127)

Biosensor
Surface plasmon resonance; BIAcore; Mass transport; Kinetics; Protein–protein interaction (Myszka, D.G. (64) 127)

Biothermodynamics
Gibbs conference (Ackers, G.K. (64) 3)

Buried ionizable group
Dielectric inside a protein; Effective dielectric; Electrostatics; pK_a in hydrophobic environment; Hydration (García-Moreno E., B. (64) 211)

Calorimetric enthalpy
Isothermal titration calorimetry; van't Hoff enthalpy (Liu, Y. (64) 121)

Calorimetry
Enthalpy; Monte Carlo simulation; Parameter estimation; van't Hoff plots (Chaires, J.B. (64) 15)

Charged ligands
Competitive electrostatic binding; Non-linear Poisson–Boltzmann equation; Polyelectrolytes (Rouzina, I. (64) 139)

Chemical denaturation
Ribonuclease A; Protein folding; Denaturant binding; Denaturant *m* values (DeKoster, G.T. (64) 59)

Chemical exchange
Protein folding; Segmental motions; NMR; Equilibrium thermodynamics (Barbar, E. (64) 45)

Competitive electrostatic binding
Charged ligands; Non-linear Poisson–Boltzmann equation; Polyelectrolytes (Rouzina, I. (64) 139)

Cooperative binding
Hemoglobin; Quaternary enhancement; Regulation; Subunit assembly (Doyle, M.L. (64) 271)

Cooperative interactions
Structural mapping; Structure-based statistical thermodynamic analysis; T4 lysozyme mutants (Hilser, V.J. (64) 69)

Cooperativity
Allosteric regulation; Hemoglobin intermediate; Subunit assembly (Huang, Y. (64) 157)

Modeling; Nonlinear analysis; Data simulation; Enzyme kinetics; GroEL (LiCata, V.J. (64) 225)

Co-solvents
Trehalose; Preferential interactions; Transfer free energy; Transfer enthalpy; Transfer entropy; Protein stabilization (Xie, G. (64) 25)

Data simulation
Cooperativity; Modeling; Nonlinear analysis; Enzyme kinetics; GroEL (LiCata, V.J. (64) 225)

Denaturant binding
Ribonuclease A; Protein folding; Chemical denaturation; Denaturant *m* values (DeKoster, G.T. (64) 59)

Denaturant *m* values
Ribonuclease A; Protein folding; Chemical denaturation; Denaturant binding (DeKoster, G.T. (64) 59)

Dielectric inside a protein
Buried ionizable group; Effective dielectric; Electrostatics; pK_a in hydrophobic environment; Hydration (García-Moreno E., B. (64) 211)

Differential scanning calorimetry
Protein unfolding; RNA binding domain; Human U1A (Lu, J. (64) 111)

Effective dielectric
Buried ionizable group; Dielectric inside a protein; Electrostatics; pK_a in hydrophobic environment; Hydration (García-Moreno E., B. (64) 211)

Electrostatics
Buried ionizable group; Dielectric inside a protein; Effective dielectric; pK_a in hydrophobic environment; Hydration (García-Moreno E., B. (64) 211)

Energetics
Fluorescence; Thermodynamics; Replication; Recombination; Repair (Ferrari, M.E. (64) 235)

Enthalpy
Calorimetry; Monte Carlo simulation; Parameter estimation; van't Hoff plots (Chaires, J.B. (64) 15)

Enzyme kinetics
Cooperativity; Modeling; Nonlinear analysis; Data simulation; GroEL (LiCata, V.J. (64) 225)

Equilibrium thermodynamics
Protein folding; Segmental motions; Chemical exchange; NMR (Barbar, E. (64) 45)

Fluorescence lifetime
Hemoglobin species; Time-resolved fluorescence (Gryczynski, Z. (64) 81)

Fluorescence quenching
Model-independent isotherms; Macromolecular binding; Helicases (Jezewska, M.J. (64) 253)

Fluorescence
Thermodynamics; Energetics; Replication; Recombination; Repair (Ferrari, M.E. (64) 235)

Gibbs conference
Biothermodynamics (Ackers, G.K. (64) 3)

Gibbs conferences
Avogadro's hypothesis; Molecular mechanisms; Site-directed mutagenesis; Thermodynamics (Schellman, J.A. (64) 7)

GroEL
Cooperativity; Modeling; Nonlinear analysis; Data simulation; Enzyme kinetics (LiCata, V.J. (64) 225)

Helicases
Model-independent isotherms; Macromolecular binding; Fluorescence quenching (Jezewska, M.J. (64) 253)

Hemoglobin
Cooperative binding; Quaternary enhancement; Regulation; Subunit assembly (Doyle, M.L. (64) 271)

Hemoglobin intermediate
Allosteric regulation; Cooperativity; Subunit assembly (Huang, Y. (64) 157)

Hemoglobin species
Fluorescence lifetime; Time-resolved fluorescence (Gryczynski, Z. (64) 81)

van't Hoff enthalpy
Calorimetric enthalpy; Isothermal titration calorimetry (Liu, Y. (64) 121)

van't Hoff plots
Enthalpy; Calorimetry; Monte Carlo simulation; Parameter estimation (Chaires, J.B. (64) 15)

Human U1A
Protein unfolding; RNA binding domain; Differential scanning calorimetry (Lu, J. (64) 111)

Hydration
Buried ionizable group; Dielectric inside a protein; Effective dielectric; Electrostatics; pK_a in hydrophobic environment (García-Moreno E., B. (64) 211)

Isothermal titration calorimetry
Calorimetric enthalpy; van't Hoff enthalpy (Liu, Y. (64) 121)

Kinetics
Surface plasmon resonance; BIAcore; Biosensor; Mass transport; Protein–protein interaction (Myszka, D.G. (64) 127)

pK_a in hydrophobic environment
Buried ionizable group; Dielectric inside a protein; Effective dielectric; Electrostatics; Hydration (García-Moreno E., B. (64) 211)

Macromolecular binding
Model-independent isotherms; Helicases; Fluorescence quenching (Jezewska, M.J. (64) 253)

Mass transport
Surface plasmon resonance; BIAcore; Biosensor; Kinetics; Protein–protein interaction (Myszka, D.G. (64) 127)

Model compounds
Scanning calorimetry; Partial heat capacity; Unfolded proteins (Makhatadze, G.I. (64) 93)

Model-independent isotherms
Macromolecular binding; Helicases; Fluorescence quenching (Jezewska, M.J. (64) 253)

Modeling
Cooperativity; Nonlinear analysis; Data simulation; Enzyme kinetics; GroEL (LiCata, V.J. (64) 225)

Molecular mechanisms
Avogadro's hypothesis; Gibbs conferences; Site-directed mutagenesis; Thermodynamics (Schellman, J.A. (64) 7)

Monte Carlo simulation
Enthalpy; Calorimetry; Parameter estimation; van't Hoff plots (Chaires, J.B. (64) 15)

Na^+
Thrombin; Allosteric enzymes; Site-directed mutagenesis (Guinto, E.R. (64) 103)

NMR
Protein folding; Segmental motions; Chemical exchange; Equilibrium thermodynamics (Barbar, E. (64) 45)

Nonlinear analysis
Cooperativity; Modeling; Data simulation; Enzyme kinetics; GroEL (LiCata, V.J. (64) 225)

Non-linear Poisson–Boltzmann equation
Charged ligands; Competitive electrostatic binding; Polyelectrolytes (Rouzina, I. (64) 139)

Parameter estimation
Enthalpy; Calorimetry; Monte Carlo simulation; van't Hoff plots (Chaires, J.B. (64) 15)

Partial heat capacity
Scanning calorimetry; Model compounds; Unfolded proteins (Makhatadze, G.I. (64) 93)

Phosphofructokinase
Phosphorylation; Self-association; Allosteric regulation; Protein–protein interaction (Cai, G.-Z. (64) 199)

Phosphorylation
Self-association; Allosteric regulation; Protein–protein interaction; Phosphofructokinase (Cai, G.-Z. (64) 199)

Polyelectrolytes
Charged ligands; Competitive electrostatic binding; Non-linear Poisson–Boltzmann equation (Rouzina, I. (64) 139)

Preferential interactions
Trehalose; Transfer free energy; Transfer enthalpy; Transfer entropy; Protein stabilization; Co-solvents (Xie, G. (64) 25)

Protein folding
Ribonuclease A; Chemical denaturation; Denaturant binding; Denaturant *m* values (DeKoster, G.T. (64) 59)

Segmental motions; Chemical exchange; NMR; Equilibrium thermodynamics (Barbar, E. (64) 45)

Protein stability
Protein unfolding; Thermodynamics; Two-state model (Eftink, M.R. (64) 175)

Protein stabilization
Trehalose; Preferential interactions; Transfer free energy; Transfer enthalpy; Transfer entropy; Co-solvents (Xie, G. (64) 25)

Protein unfolding
Protein stability; Thermodynamics; Two-state model (Eftink, M.R. (64) 175)

RNA binding domain; Human U1A; Differential scanning calorimetry (Lu, J. (64) 111)

Protein–protein interaction
Phosphorylation; Self-association; Allosteric regulation; Phosphofructokinase (Cai, G.-Z. (64) 199)

Surface plasmon resonance; BIAcore; Biosensor; Mass transport; Kinetics (Myszka, D.G. (64) 127)

Quaternary enhancement
Cooperative binding; Hemoglobin; Regulation; Subunit assembly (Doyle, M.L. (64) 271)

Recombination
Fluorescence; Thermodynamics; Energetics; Replication; Repair (Ferrari, M.E. (64) 235)

Regulation
Cooperative binding; Hemoglobin; Quaternary enhancement; Subunit assembly (Doyle, M.L. (64) 271)

Repair
Fluorescence; Thermodynamics; Energetics; Replication; Recombination (Ferrari, M.E. (64) 235)

Replication
Fluorescence; Thermodynamics; Energetics; Recombination; Repair (Ferrari, M.E. (64) 235)

Ribonuclease A
Protein folding; Chemical denaturation; Denaturant binding; Denaturant *m* values (DeKoster, G.T. (64) 59)

RNA binding domain
Protein unfolding; Human U1A; Differential scanning calorimetry (Lu, J. (64) 111)

Scanning calorimetry
Partial heat capacity; Model compounds; Unfolded proteins (Makhatadze, G.I. (64) 93)

Segmental motions
Protein folding; Chemical exchange; NMR; Equilibrium thermodynamics (Barbar, E. (64) 45)

Self-association
Phosphorylation; Allosteric regulation; Protein–protein interaction; Phosphofructokinase (Cai, G.-Z. (64) 199)

Site-directed mutagenesis
Avogadro's hypothesis; Gibbs conferences; Molecular mechanisms; Thermodynamics (Schellman, J.A. (64) 7)

Thrombin; Allosteric enzymes; Na^+ (Guinto, E.R. (64) 103)

Structural mapping
Cooperative interactions; Structure-based statistical thermodynamic analysis; T4 lysozyme mutants (Hilser, V.J. (64) 69)

Structure-based statistical thermodynamic analysis
Cooperative interactions; Structural mapping; T4 lysozyme mutants (Hilser, V.J. (64) 69)

Subunit assembly
Allosteric regulation; Cooperativity; Hemoglobin intermediate (Huang, Y. (64) 157)

Cooperative binding; Hemoglobin; Quaternary enhancement; Regulation (Doyle, M.L. (64) 271)

Surface plasmon resonance
BIAcore; Biosensor; Mass transport; Kinetics; Protein–protein interaction (Myszka, D.G. (64) 127)

T4 lysozyme mutants
Cooperative interactions; Structural mapping; Structure-based statistical thermodynamic analysis (Hilser, V.J. (64) 69)

Thermodynamics
Avogadro's hypothesis; Gibbs conferences; Molecular mechanisms; Site-directed mutagenesis (Schellman, J.A. (64) 7)

Fluorescence; Energetics; Replication; Recombination; Repair (Ferrari, M.E. (64) 235)

Protein stability; Protein unfolding; Two-state model (Eftink, M.R. (64) 175)

Thrombin
Allosteric enzymes; Na^+; Site-directed mutagenesis (Guinto, E.R. (64) 103)

Time-resolved fluorescence
Fluorescence lifetime; Hemoglobin species (Gryczynski, Z. (64) 81)

Transfer enthalpy
Trehalose; Preferential interactions; Transfer free energy; Transfer entropy; Protein stabilization; Co-solvents (Xie, G. (64) 25)

Transfer entropy
Trehalose; Preferential interactions; Transfer free energy; Transfer enthalpy; Protein stabilization; Co-solvents (Xie, G. (64) 25)

Transfer free energy
Trehalose; Preferential interactions; Transfer enthalpy; Transfer entropy; Protein stabilization; Co-solvents (Xie, G. (64) 25)

Trehalose
Preferential interactions; Transfer free energy; Transfer enthalpy; Transfer entropy; Protein stabilization; Co-solvents (Xie, G. (64) 25)

Two-state model
Protein stability; Protein unfolding; Thermodynamics (Eftink, M.R. (64) 175)

Unfolded proteins
Scanning calorimetry; Partial heat capacity; Model compounds (Makhatadze, G.I. (64) 93)